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(FILE 'HOME' ENTERED AT 09:35:01 ON 25 APR 2007)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT 09:36:18 ON 25 APR 2007

L1 99 SEA ABB=ON PLU=ON ALICYCLOBACILLUS AND PCR
L2 16 SEA ABB=ON PLU=ON L1 AND REAL-TIME
L3 7 DUP REM L2 (9 DUPLICATES REMOVED)
DIS 33 1-7 IBIB
DIS L3 2-7 IBIB
L4 13 SEA ABB=ON PLU=ON L1 AND TAQMAN
DIS L4 ALL IBIB
DIS L4 2-14 IBIB
L5 51 SEA ABB=ON PLU=ON L1 AND 16S
L6 22 DUP REM L5 (29 DUPLICATES REMOVED)
DIS L6 1-22 IBIB

FILE 'STNGUIDE' ENTERED AT 09:48:01 ON 25 APR 2007

FILE HOME

FILE MEDLINE

FILE LAST UPDATED: 24 Apr 2007 (20070424/UP). FILE COVERS 1950 TO DATE.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE BIOSIS

FILE COVERS 1969 TO DATE.

CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 18 April 2007 (20070418/ED)

FILE CAPLUS

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FILE COVERS 1907 - 25 Apr 2007 VOL 146 ISS 18

FILE LAST UPDATED: 24 Apr 2007 (20070424/ED)

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FILE EMBASE

FILE COVERS 1974 TO 24 Apr 2007 (20070424/ED)

EMBASE is now updated daily. SDI frequency remains weekly (default) and biweekly.

This file contains CAS Registry Numbers for easy and accurate

substance identification.

FILE SCISEARCH

FILE COVERS 1974 TO 19 Apr 2007 (20070419/ED)

SCISEARCH has been reloaded, see HELP RLOAD for details.

FILE AGRICOLA

FILE COVERS 1970 TO 3 Apr 2007 (20070403/ED)

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FILE STNGUIDE

FILE CONTAINS CURRENT INFORMATION.

LAST RELOADED: Apr 20, 2007 (20070420/UP).

=>

Sequence Alignments.

113

1. Sequence alignment of Hristova's primers and probes to the PM1 16S ribosomal RNA gene alignment

```
963F 1 CCTTGACATGTCTAGAAAGTTACCAGAGA 28
      |||||||||||||||||||||||||
16S 963 CCTTGACATGTCTAGAAAGTTACCAGAGA 990
```

```
1076R 1 GCGGGACTTAACCCAACATCT 21
      |||||||||||||||||||||
16s 1076 GCGGGACTTAACCCAACATCT 1056
```

```
1030T 1 ACACGAGCTGACGACGGCCATG 22
      |||||||||||||||||||||
16S 1011 ACACGAGCTGACGACGGCCATG 990
```

2. Sequence alignments of 10/727261 SEQ ID NOs: 1, 2 and 4:

RESULT 9 (SEQ ID NO: 1) FORWARD PRIMER

ID ADW05721

```
Qy 1 GAGCCCGCGGCGCATTAGC 19
    |||||||||||||||||||
Db 214 GAGCCCGCGGCGCATTAGC 232
```

RESULT 27 (SEQ ID NO: 4) REVERSE PRIMER

ADW05721/c

```
Qy 1 GCTTGCGCCCATTGCG 16
    |||||||||||||||||
Db 369 GCTTGCGCCCATTGCG 354
```

RESULT 76 (SEQ ID NO: 2) PROBE

ADW05721

```
Qy 1 GCGACGATGCGTAGCCG 17
    |||||||||||||||||
Db 260 GCGACGATGCGTAGCCG 276
```

3. SEQ ID NO:78. (10/727/261) and Alicyclobacillus and Geobacillus rDNA alignments, and SEQ ID NOs: 1,2 and 4 alignments. See pages (2-9).

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x dropoff: 0 expect: 10.0000 wordsize: 11 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation

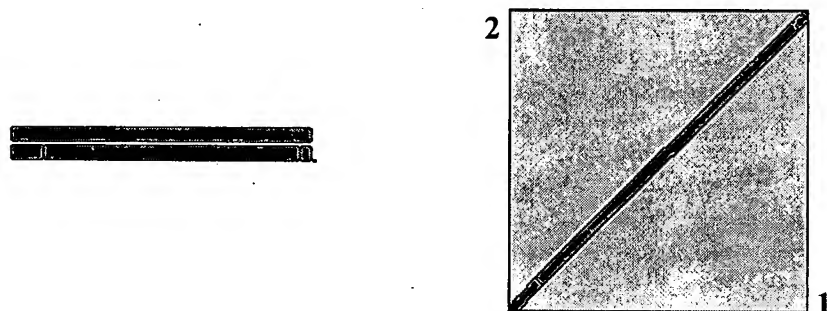
Sequence 1: lcl|seq 1

Length = 1498 (1 .. 1498)

SEQ 10 # 70

④ **Sequence 2:** [gi|18496336|dbj|AB042058.1](https://www.ncbi.nlm.nih.gov/nuclot/gi|18496336|dbj|AB042058.1)|*Alicyclobacillus acidoterrestris* gene for 16S ribosomal RNA, partial sequence.

Length = 1514 (1 .. 1514)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 2619 bits (1362), Expect = 0.0
Identities = 1450/1498 (96%), Gaps = 3/1498 (0%)
Strand=Plus/Plus

Query	1	AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGC	60
Sbjct	1	AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGC	60
Query	61	GGGCCCTTCGGGGCCAGCGGCGGACGGGTGAGTAACACGTGGGTAATCTGCCTTTTCAGAC	120
Sbjct	61	GAGCCCTTCGGGGCTAGCGGCGGACGGGTGAGTAACACGTGGGCAATCTGCCTTTTCAGAC	120
Query	121	CGGAATAACGCCCGAAACGGGTGCTAATGCCGGATANGCACGCGAGNAGGCATCTNCTT	180

Query	Sbjct	Seq ID # 1 Forward	prim
Query 121	TGGAATAACACTCGGAAACGGGTGCTAATGCCGGATAAT-ACACGGGTAGGCATCTACTT	179	
Query 181	GCGGGGAAAGGTGCAANTGCATCGCTGAGAGAGGAGCCCGCGGCGCATTAGCTAGTTGGT	240	
Sbjct 180	GTGTTGAAAGATGCAACTGCATCGCTGAGAGAGGAGCCCGCGGCGCATTAGCTAGTTGGT	239	
Query 241	GGGGTAACGGCTCACCAAGCGACGATGCGTAGCCGACCTGAGAGGGTGACCGGCCACAC	300	
Sbjct 240	GAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGACCGGCCACAC	299	
Query 301	TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATG	360	
Sbjct 300	TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATG	359	
Query 361	GGCGCAAGCCTGACGGAGCAACGCCGCGTGAGCGAAGAAGGCCTTCGGGTTGTAAAGCTC	420	
Sbjct 360	GGCGCAAGCCTGACGGAGCAACGCCGCGTGAGCGAAGAAGGCCTTCGGGTTGTAAAGCTC	419	
Query 421	TGTTGCTCGGGGAGAGCGGCAAGGGGAGTGAAAGCCCCTTGNGAGACGGTACCGAGTGA	480	
Sbjct 420	TGTTGCTCGGGGAGAGCGGCAAGGGGAGTGAAAGCTCCTTGAGACGGTACCGAGTGA	479	
Query 481	GGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTC	540	
Sbjct 480	GGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTC	539	
Query 541	CGGAATCACTGGGCGTAAAGCGTGCGTAGGCGGTTGNGTAAGTCTGGAGTGAAAGTCCAN	600	
Sbjct 540	CGGAATCACTGGGCGTAAAGCGTGCGTAGGCGGTTGTGTAAGTCTGAAGTGAAAGTCCAA	599	
Query 601	GGCTCAACCNCTGGGAATGCTTTGGAACTGCNTGACTTGAGTGCTGGAGAGGCAAGGGGA	660	
Sbjct 600	GGCTCAACCNCTGGGAATGCTTTGGAACTGCNTGACTTGAGTGCTGGAGAGGCAAGGGGA	659	
Query 661	ATTCCNCGTGAGCGGTGNAATGCGTAGATATGTGGAGGAATACCAAGTGGCGAANGCGCC	720	
Sbjct 660	ATTCCACGTGAGCGGTGAAATGCGTAGATATGTGGAGGAATACCAAGTGGCGAANGCGCC	719	
Query 721	TTGCTGGACAGTGACTGACGCTGAGGCACGAAAGCGTGAGGAGCAAACAGGATTAGATAC	780	
Sbjct 720	TTGCTGGACAGTGACTGACGCTGAGGCACGAAAGCGTGAGGAGCAAACAGGATTAGATAC	779	
Query 781	CCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGGGGACACACCCCAGTGCC	840	
Sbjct 780	CCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGGGGACACACCCCAGTGCC	839	
Query 841	GAAGGAAACCCAATAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGG	900	
Sbjct 840	GAAGGAAACCCAATAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGG	899	
Query 901	AATTGACGGGGGCGCACAAAGCAGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGA	960	
Sbjct 900	AATTGACGGGGGCGCACAAAGCAGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGA	959	
Query 961	ACCTTACCAGGGCTNGACATCCCTCTGACAGCCGAGAGATGNGGNTTCCCTTCGGGGCA	1020	
Sbjct 960	ACCTTACCAGGGCTNGACATCCCTCTGACAGCCGAGAGATGNGGNTTCCCTTCGGGGCA	1019	
Query 1021	GAGGAGACAGGTGGTGCATGGTTGTCGTGAGTGTGTCGTGAGATGTTGGGTTAAGTCC	1080	